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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 19:31:40 ; Search time 129 seconds
(without alignments)
5173.090 Million cell updates/sec

Title: PCT-US02-16639-1

Perfect score: 2176

Sequence: 1 attgtgtcaggttggtgggc.....taggtgcaggttgcaaaa 2176

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*

2: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*

3: /cgn2.6/ptodata/1/ina/6A.COMB.seq.*

4: /cgn2.6/ptodata/1/ina/6B.COMB.seq.*

5: /cgn2.6/ptodata/1/ina/PCTUS.COMB.seq.*

6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	47.8	2.2	7218	1	US-08-232-463-14	Sequence 14, Appl
2	37.8	1.7	548	3	US-08-828-741B-1	Sequence 1, Appl
3	37.8	1.7	548	4	US-09-160-567-1	Sequence 1, Appl
C 4	35.4	1.6	1690	1	US-08-276-452A-24	Sequence 24, Appl
C 5	35.4	1.6	1690	2	US-08-798-744-24	Sequence 24, Appl
6	34.8	1.6	993	4	US-09-134-001C-745	Sequence 745, App
7	32.8	1.5	499	4	US-09-328-111-97	Sequence 97, Appl
8	32.6	1.5	964	3	US-08-755-587-23	Sequence 23, Appl
9	32.6	1.5	1041	3	US-08-755-587-22	Sequence 22, Appl
10	32.6	1.5	1050	3	US-08-755-587-21	Sequence 21, Appl
C 11	32.6	1.5	1432	5	PCT-US94-12912-4	Sequence 4, Appl
12	32.6	1.5	4770	4	US-09-000-094-45	Sequence 45, Appl
13	32.6	1.5	8010	4	US-09-521-526-2	Sequence 2, Appl
14	32.6	1.5	8010	5	PCT-US95-1189-2	Sequence 2, Appl
C 15	32.4	1.5	4550	4	US-09-462-136-1	Sequence 1, Appl
C 16	32.2	1.5	4253	3	US-08-577-483-7	Sequence 7, Appl
C 17	32.2	1.5	4254	2	US-08-443-639-7	Sequence 7, Appl
18	32	1.5	1031	3	US-08-828-741B-5	Sequence 5, Appl
19	32	1.5	1031	4	US-09-160-567-5	Sequence 5, Appl
20	32	1.5	1490	3	US-08-828-741B-3	Sequence 3, Appl
21	32	1.5	1490	4	US-09-160-567-3	Sequence 3, Appl
22	32	1.5	1939	4	US-08-961-527-310	Sequence 310, App
23	31.8	1.5	4233	4	US-09-056-103-27	Sequence 27, Appl
24	31.6	1.5	84495	4	US-09-797-906-3	Sequence 3, Appl
25	31.4	1.4	2277	1	US-08-676-967-2	Sequence 2, Appl
26	31.4	1.4	2277	1	US-08-676-974-2	Sequence 2, Appl
27	31.4	1.4	2277	2	US-09-098-487-2	Sequence 2, Appl

28	31.4	1.4	6393	4	US-09-323-872A-8	Sequence 8, Appl
29	31.2	1.4	155	1	US-07-626-618A-12	Sequence 12, Appl
30	31.2	1.4	155	1	US-08-333-977-12	Sequence 12, Appl
31	31.2	1.4	539	3	US-08-828-741B-12	Sequence 12, Appl
32	31.2	1.4	539	4	US-09-160-567-12	Sequence 12, Appl
33	31.2	1.4	563	1	US-07-928-611-8	Sequence 8, Appl
34	31.2	1.4	563	2	US-08-487-811A-8	Sequence 8, Appl
35	31.2	1.4	563	4	US-09-060-694-8	Sequence 8, Appl
36	31.2	1.4	563	4	US-09-378-074-8	Sequence 8, Appl
37	31.2	1.4	563	5	PCT-US93-07370-8	Sequence 8, Appl
38	31.2	1.4	599	3	US-08-828-741B-7	Sequence 7, Appl
39	31.2	1.4	599	4	US-09-160-567-7	Sequence 7, Appl
40	31.2	1.4	659	1	US-07-928-611-10	Sequence 10, Appl
41	31.2	1.4	659	2	US-08-487-811A-10	Sequence 10, Appl
42	31.2	1.4	659	4	US-09-060-694-10	Sequence 10, Appl
43	31.2	1.4	659	4	US-09-378-074-10	Sequence 10, Appl
44	31.2	1.4	659	5	PCT-US93-07370-10	Sequence 10, Appl
45	31.2	1.4	803	1	US-07-928-611-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)833-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; CLONE: PT29pt-F1s
; IMMEDIATE SOURCE:
; US-08-232-463-14

Query Match 2.2%; Score 47.8; DB 1; Length 7218;


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; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 745
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-745

Query Match 1.6%; Score 34.8; DB 4; Length 993;
Best Local Similarity 54.8%; Pred. No. 0.9;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 770 TAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACATGGAGAAAGTTGTACATCGAA 829
Db 419 TTACTTTAGTAGTACGGGCTAGTGGAGGTATATTTCTAATGGAGAAATTTGTACATGGAC 478
QY 830 TGCACACAGTACACACAGTATATACGTCCTTTTAAATGGCAAAATTTTATCCCAAGTGTATCCA 889
Db 479 ACAATGGTCTCGCGCTGAGATGGACATTTAAGAGCGTGAATTTTATGATCAACAGTTTTCAT 538
QY 890 GAAATT 895
Db 539 GCAATT 544

RESULT 7
US-09-328-111-97
; Sequence 97, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(499)
; OTHER INFORMATION: n = A,T,C or G
; US-09-328-111-97

Query Match 1.5%; Score 32.8; DB 4; Length 499;
Best Local Similarity 59.8%; Pred. No. 2.5;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1347 GGACTGGGTGCACAGTGGATGCCGGAAGAGGTACAGTCAAAAGAGAGATGTGTGAGAA 1406
Db 23 GGACTGGGTGCACAGTGGAGCCCTGGACAGCATCCCTCTGCAGAGAGAGATTTGTCTG 82

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QY 1407 GACAGGCCAGGAGAGCATCTCAAACTACCA 1438
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Dδ 83 GCCAGAGCCTGGAGAAGCTGAAGAAGACCA 114

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RESULT 8
US-08-755-587-23
; Sequence 23, Application US/08755587
; Patent No. 6045997
; GENERAL INFORMATION:
; APPLICANT: Futreal, Phillip A
; APPLICANT: Wooster, Richard F
; APPLICANT: Ashworth, Alan
; APPLICANT: Stratton, Michael R
; TITLE OF INVENTION: Materials and methods relating to the
; TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
; TITLE OF INVENTION: susceptibility gene and uses thereof.

```

```

? NUMBER OF SEQUENCES: 222
? CORRESPONDENCE ADDRESS:
? ADDRESS: Bell Seltzer Park & Gibson
? STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
? CITY: Raleigh
? STATE: NC
? COUNTRY: USA
?

```

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/ COORDINATE: 0000
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/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,587
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:

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: APPLICATION NUMBER:  GB 9523959.6
: FILING DATE: 23-NOV-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:  GB 9525555.0
: FILING DATE: 14-DEC-1995
:
:

```

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9617961.9
 ; FILING DATE: 28-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ;

```

; NAME: Kenneth D Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-135
; INFORMATION FOR SEQ ID NO: 23:

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SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
TYPE: nucleic acid
STAMPEDNESS: double

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1 STRANDEDNESS: double
2
3 TOPOLOGY: linear
4
5 MOLECULE TYPE: DNA (genomic)
6
7 FEATURE:
8
9 NAME/GENE: CDC

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/ NAME/KEY: CDS
/ LOCATION: 501..615
/ FEATURE:
/ NAME/KEY: exon 5

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; LOCATION: 501.615
US-08-755-587-23

Query Match      1.5%; Score 32.6; DB 3; Length 964;

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QY 646 CTGTGGTTCACATAGACAGCAAAATCGAAAAAGACAAAGTGAAGATTACCGGGATCACTTTC
 Best Local Similarity 46.0%; Pred. No. 4.4;
 Matches 110; Conservative 0; Mismatches 129; Indels 0; Gaps

Db	105	CTGTGTTTCTACAATGTACACATGTACACACACAAAGAGATAAGTCAGGTATGATTTAAAA
QY	706	AACACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCATTTTATGGTCAT

Db 165 ACAATGCITTTTATTCITAGAACTACTAGAATGTTATATAAAATAAAGCTTACCAATTTT

Db 422 ACAATGCTTTTATCTTGAATAGTACGAAATGTTAAATAAAATTAACAAATTTT 481
Qy 766 TTCTAAATGAAGTCACTGCGCACTGGGGTTTCATATATCTGAGAGAGTTGTACAT 825
Db 482 CCCCTTTTATCCCACTGATGTGGAGTTTGTTCATACACCAAAATTTGTGAAG 541
Qy 826 CGAATGCTCACAGCTACACATATATAGCTCCCTTTAATGGCAAAATTTTGATCCCAAGT 884
Db 542 GTAATATTCTACTGCTGTTATTTTATGACTAGTAAATGAGAAATTTGACAATAGCT 600

RESULT 10

US-08-755-587-21

; Sequence 21, Application US/08755587

; Patent No. 6045997

; GENERAL INFORMATION:

; APPLICANT: Futreal, Phillip A

; APPLICANT: Wooster, Richard F

; APPLICANT: Ashworth, Alan

; APPLICANT: Stratton, Michael R

; TITLE OF INVENTION: Materials and methods relating to the

; TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer

; TITLE OF INVENTION: susceptibility gene and uses thereof.

; NUMBER OF SEQUENCES: 222

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bell Seltzer Park & Gibson

; STREET: 310 JCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107

; CITY: Raleigh

; STATE: NC

; COUNTRY: USA

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/755,587

; FILING DATE: 25-NOV-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9523959.6

; FILING DATE: 23-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9525555.0

; FILING DATE: 14-DEC-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9617961.9

; FILING DATE: 28-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Kenneth D Sibley

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5405-135

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1050 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 502..550

; FEATURE:

; NAME/KEY: exon

; LOCATION: 501..550

; US-08-755-587-21

Query Match 1.5%; Score 32.6; DB 3; Length 1050;

Best Local Similarity 46.0%; Pred. No. 4.7;

Matches 110; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

Qy 646 CTGTGGGTAACTAGACCAATCGAAAAAGACAAAGTGAAGATTCACGGATCTTCC 705

Db 503 CTGTTGTTTCTACAATGTACACATGTACACACCAAGAGATAAGTCAGGTATGATTTAAA 562
Qy 706 AACACTCATCGGCAAGCTGCAAGAGTGAATCTGCTCTTCGATTTTCCATTTTATGGTCAT 765
Db 563 ACAATGCTTTTATCTTCTAGATACTAGAAATGTTAATAAAATAAAACTTAACAATTT 622
Qy 766 TTCTAAATGAAGTCACTGTCGCACTGGGGTTTCATATATCTGAGAGAGTTGTACAT 825
Db 623 CCCCTTTTATCCCACTGATGTGGAGTTTGTTCATACACCAAAATTTGTGAAG 682
Qy 826 CGAATGCTCACAGCTACACAGTATATAGCTCCCTTTAATGGCAAAATTTTGATCCCAAGT 884
Db 683 GTAATATTCTACTGCTGTTATTTTATGACTAGTAAATGAGAAATTTGACAATAGCT 741

RESULT 11

PCT-US94-12912-4/c

; Sequence 4, Application PC/TUS9412912

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: TRANSDUCTION OF CELLS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: C/O Robbins, Berliner & Carson

; STREET: 201 North Figueroa Street, Fifth Floor

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/12912

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Spitals, John P.

; REGISTRATION NUMBER: 29,215

; REFERENCE/DOCKET NUMBER: 1920-341

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 977-1001

; TELEFAX: (213) 977-1003

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; PCT-US94-12912-4

Query Match 1.5%; Score 32.6; DB 5; Length 1432;

Best Local Similarity 46.0%; Pred. No. 5.8;

Matches 110; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

Qy 1192 AAAATTACCAATCTCAGCTGTGGAGATGATCTCCCACTTCCCACTGTCCTCCAGTTCAT 1251

Db 940 AATCTTACAAATTTACAACTGAAAGAAATCTTTATGTACATGTTCTCTGTTGGGA 981

Qy 1252 GGTGTGCGCTTGTGTGTCCTCGAGATGTTTCAACTGCGAGTTGGTGGCAGCAAACTT 1311

Db 880 CTTTGTGAAGCCTTCTTCGTCCTGTGTATTAGGCCCTCCCTGGAGAGTCATATAGACCA 821

Qy 1312 CAAAGATGCTCCAGTGGATTTGATCGCCATCGGACAGACTGGGTGGACAGTGGATCCCG 1371

Db 820 GAAATATTAGTTCATAGCACATGATAGTAAGCCTGGAACCTAGAAAGCCCTGGAGTTGAG 761

Qy 1372 GAAAGGTACAGTCAAAGAGAGAGATGTGTGAGAAGACAGAGCCAGGAGAGATCTCA 1430

Db 3354 AGCGCCCAAAACAGTGTACGGGAGCATGCA 3384

RESULT 13

US-09-521-526-2

; Sequence 2, Application US/09521526

; Patent No. 6290965

; GENERAL INFORMATION:

; APPLICANT: JANSEN, KATHRIN U.

; APPLICANT: HOFMANN, KATHRYN J.

; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE

; TITLE OF INVENTION: 6A

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHRISTINE E. CARTY

; STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000

; CITY: RAHWAY

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065-0900

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/521,526

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/310,468

; FILING DATE: 22-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CARTY, CHRISTINE E.

; REGISTRATION NUMBER: 36,099

; REFERENCE/DOCKET NUMBER: 19307

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 594-6734

; TELEFAX: (908) 594-4720

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8010 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-521-526-2

Query Match 1.5%; Score 32.6; DB 4; Length 8010;

Best Local Similarity 51.0%; Pred.No.18; Mismatches 0; Gaps 0;

Matches 77; Conservative 0; Indels 74;

QY 405 TGAAGAGGGGGTAGAAGTGGACTCTCAAGCATCAACCCACAGCGTGGAAAGAAATGTGGA 464

Db 1252 TGAAGTGAAGCTGGAGCGGGAACGCAGGTAGAGAAACATGGCGTCCCGGAAAATGGGGG 1311

QY 465 CCCTTTTAAAGCAGTAGACACAAACAGGCCAGCATGGGCCACAGCCTCTCCAGAGTCCAA 524

Db 1312 AGATGTCAGGAAAGGACACAGGAAGGGACATAGAGGGGGAGGAACATACAGAGGGCGGA 1371

QY 525 AGGGTTCACTGACCTGCTACTTGGATGACGGA 555

Db 1372 AGCGCCCAACACAGTGTACGGGAGCATGCA 1402

RESULT 14

PCT-US95-11859-2

; Sequence 2, Application PC/TUS9511859

; GENERAL INFORMATION:

; APPLICANT: JANSEN, KATHRIN U.

; APPLICANT: HOFMANN, KATHRYN J.

; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE

TITLE OF INVENTION: 6A
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHRISTINE E. CARTY
 STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000
 CITY: RAYWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11859
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/310,468
 FILING DATE: 22-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: CARTY, CHRISTINE E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 19307 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8010 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 PCT-US95-11859-2

	Query Match	1.5%	Score 32.6;	DB 5;	Length 8010;
	Best Local Similarity	51.0%;	Pred. No. 18;		
Matches	77; Conservative	0;	Mismatches 74;	Indels 0;	Gaps 0;
QY	405	TGAAGAGGGGTAGAAGTGGACTCTCAGCATACAAACACAGGTTGGAAAAGAAATGTGGA	464		
Ddb	1252	TGAAGTGGAAGCTTGGAACGGGACGCAGGTAGAGAAACATGGCGTCCCGGAAATATGGGG	1311		
QY	465	CCCTTTTTAAGCGTAGTAGACAACAGACCAGCATGGGCCAAGCCTCTCCAGAGTCCAA	524		
Ddb	1312	AGATGGTCAGAAAGGACACAGGAAGGACATAGAGGGGGAGGNACATACAGAGGGCGA	1371		
QY	525	AGGTTCACTGACCTGCTACTCGATGAACGA	555		
Ddb	1372	AGCCCCACAAACAGTGTACGGGAGCATGCA	1402		

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RESULT 15
US-09-462-136-1/c
; Sequence 1, Application US/09462136
; Patent NO. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstee, et al.
; TITLE OF INVENTION: Genes for Nicotian-Pick Type C Disease
; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4550
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3837)
US-09-462-136-1

Query Match          1.5%; Score 32.4; DB 4; Length 4550;
Best Local Similarity 47.5%; Pred. No.14;
Matches 96; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY      1689 GTATCACCATCCAAATCATCAGCCAGCAGCATCTTCTTCATTGAGAGACGCCCAAGCAGATG 1748
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QY      1749 GCCAGCAATGAATTTTCGAGAGGGTTCAGGACACCCCTGCCTATGCAAGAGTTGAACCAGT 1808
Dbb     961 CCTCTCTTTGTCTCACTTGCATTAAACAGAAAAAGCTATATTGCTATCCATGGGAGTGTACT 902
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Search completed: June 23, 2003, 22:05:47
Job time : 131 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 17:38:49 ; Search time 486 Seconds
(without alignments)
10083.021 Million cell updates/sec

Title: PCT-US02-16639-1

Perfect score: 2176

Sequence: 1 attgtgtctcagttggggc.....taggtgcagggttgcacaaa 2176

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1935.6	89.0	2009	24	ABL92084
2	1935.6	89.0	2010	24	ABL92137
3	1478.2	67.9	2817	22	AAH5224
4	1476.6	67.9	2594	22	AAH46160
5	1440.4	66.2	3095	22	AAH23066
6	1423.8	65.4	2157	24	ABL92080
7	1423.8	65.4	2159	24	ABL92088
8	1423.4	65.4	2557	22	AAH87054
9	1238	56.9	1590	22	AAH23067

C	10	1195.2	54.9	2668	22	AAI60009	Human polynucleoti
C	11	1195.2	54.9	2668	22	AAI60010	Human polynucleoti
	12	1195.2	54.9	2668	22	AAH75398	Human polynucleoti
	13	1195.2	54.9	2668	22	AAH23063	Stem cell growth f
	14	1195.2	54.9	2668	22	AAH23064	Stem cell growth f
	15	1165.2	53.5	2275	22	AAI58223	Human polynucleoti
	16	1031.6	47.4	1351	22	AAH23068	Stem cell growth f
	17	951.8	43.7	1179	22	AAH23065	Stem cell growth f
	18	806	37.0	1252	22	AAH14197	Human cDNA sequenc
	19	727.8	33.4	1101	21	AAH74708	Human ORFX ORF263
	20	393.6	18.1	2320	24	ABL92103	Human Tumour Endot
	21	393.6	18.1	4640	24	ABL92077	Human Tumour Endot
	22	384.4	17.7	494	22	AAH23054	Stem cell growth f
	23	365.6	16.8	2833	24	ABL92083	Mouse Tumour Endot
	24	365.6	16.8	2840	24	ABL92136	Mouse Tumour Endot
	25	347.6	16.0	1201	21	AAH77340	Human ORFX ORF2895
C	26	343.6	15.8	406	22	AAH23062	Stem cell growth f
	27	333	15.3	820	22	AAH93283	Human tumour endot
	28	333	15.3	820	22	AAH93285	Human tumour endot
C	29	328.6	15.1	392	22	AAH23051	Stem cell growth f
	30	328.4	15.1	412	22	AAH23058	Stem cell growth f
	31	322.4	14.8	498	22	AAH23048	Human immune/haema
	32	321.8	14.8	1141	22	AAH61650	Human cDNA clone (
	33	318.6	14.6	479	22	AAH05765	Human cell growth f
	34	298	13.7	366	22	AAH23042	Stem cell growth f
C	35	295	13.6	382	22	AAH23061	Stem cell growth f
	36	290	13.3	417	22	AAH23052	Stem cell growth f
C	37	275.2	12.6	416	22	AAH23060	Stem cell growth f
	38	269.2	12.4	430	22	AAH23056	Human breast cance
	39	266.6	12.3	348	22	AAH22512	Stem cell growth f
	40	266	12.2	334	22	AAH23043	Human breast cance
	41	265.6	12.2	347	22	AAH13643	Human breast cance
	42	260.6	12.0	415	22	AAH23053	Stem cell growth f
	43	231.4	10.6	534	22	AAH93287	Human tumour endot
	44	229.8	10.6	323	24	ABN17873	Human ORFX polynuc
	45	217.8	10.0	422	22	AAH23044	Stem cell growth f

ALIGNMENTS

RESULT 1

ABL92084
ID ABL92084 standard; cDNA; 2009 BP.

XX AC ABL92084;

XX DT 30-MAY-2002 (first entry)

XX DE Mouse Tumour Endothelial Marker polynucleotide SEQ ID NO 185.

XX DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;

KW normal endothelial marker; pan-endothelial marker; immunostimulant;

KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;

KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;

KW psoriasis; gene; ss.

XX OS Mus musculus.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US24031.

XX PR 02-AUG-2000; 2000US-222599P.

XX PR 11-AUG-2000; 2000US-224360P.

XX PR 11-APR-2001; 2001US-282850P.

XX PA (UJJO) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzier KW, Vogelstein B;

XX

Db 1741 CAGAGGGCGAGAGATTTCCTGGACAGCCAGCCAGAACATGTGAAGAGAAACTCAG 1800
QY 2035 ACTTGTAAGACACCATGTCAATGATTAAAGAAATCCCTAGTGGAAATGACATCCATGG 2094
Db 1801 ACTTGTAAGACACCATGTCAATGATTAAAGAAATCCCTAGTGGAAATGACATCCATGG 1860
QY 2095 TTCACAAGAACATCTCCGGTGGACTTCCAGGAGTGTGACGAGATGACATGCTTTTGG 2154
Db 1861 TTCACAAGAACATCTCCGGTGGACTTCCAGGAGTGTGACGAGATGACATGCTTTTGG 1920
QY 2155 TTTAGTGCAGGGTTGCAAAA 2176
Db 1921 TTTAGTGCAGGGTTGCAAGA 1942

RESULT 2
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ID ABL92137 standard; cDNA; 2010 BP.
XX
AC ABL92137;
XX
DT 30-MAY-2002 (first entry)
XX
DE Mouse Tumour Endothelial Marker polynucleotide SEQ ID NO 298.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neovascularization; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
XX
OS Mus musculus.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US24031.
XX
PR 02-AUG-2000; 2000US-222599P.
PR 11-AUG-2000; 2000US-224360P.
PR 11-APR-2001; 2001US-282850P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
DR P-PSDB; ABB90784.
DR
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth -
XX
XX Disclosure; Page 302-303; 331pp; English.
PS
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neovascularization in
CC subjects bearing a vascularised tumour, polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX
XX Sequence 2010 BP; 625 A; 461 C; 475 G; 449 T; 0 other;
SQ

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1938; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 295 GTATGTTACTTGTCTACTTTTAAACAGACGGTTCAGTTCGCCACGGGGAGCCTGGA 354
Db 61 GTATGTTACTTGTCTACTTTTAAACAGACGGTTCAGTTCGCCACGGGGAGCCTGGA 120
QY 355 CACCATACCAATGATTGGATTATGAAGTTACAACGCTTTTCCTTGGATGAAGAGGGG 414
Db 121 CACCATACCAATGATTGGATTATGAAGTTACAACGCTTTTCCTTGGATGAAGAGGGG 180
QY 415 GTAGAAGTGGACTCTCAAGCATACAACACAGGTGGAAGAAATGTGGACCCCTTTTAA 474
Db 181 GTAGAAGTGGACTCTCAAGCATACAACACAGGTGGAAGAAATGTGGACCCCTTTTAA 240
QY 475 GCAGTAGACACAACAGAGCCAGCATGGCCAAAGCTCTCCAGAGTCCAAAGGGTTCAT 534
Db 241 GCAGTAGACACAACAGAGCCAGCATGGCCAAAGCTCTCCAGAGTCCAAAGGGTTCAT 300
QY 535 GACCTGCTACTGGATGACGAGCAGGACAATAACCCAGATAGAGGAGGACACGGATCAC 594
Db 301 GACCTGCTACTGGATGACGAGCAGGACAATAACCCAGATAGAGGAGGACACGGATCAC 360
QY 595 AATTACTACATTTCTCGATATATGTTCCAGCGGATTTCTGCCACCCGGGATCTGTGGGTT 654
Db 361 AATTACTACATTTCTCGATATATGTTCCAGCGGATTTCTGCCACCCGGGATCTGTGGGTT 420
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Db 421 AACATAGACCAATGGAAGAAAGACAAGTGAAGATTCACGGGATCTTCCAAACACTCAT 480
QY 715 CGGCAAGTGCAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGTCATTTTCTAAAT 774
Db 481 CGGCAAGTGCAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGTCATTTTCTAAAT 540
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QY 835 ACAGTACACAGTATATAGCTCCTTTAATGCAAAATTTTGATCCAGTGTATCCAGAAAT 894
Db 601 ACAGTACACAGTATATAGCTCCTTTAATGCAAAATTTTGATCCAGTGTATCCAGAAAT 660
QY 895 TCAACTGTCCAGATATTTGATAATGGCAGCTTCTGTTCCAGTGGGACCATGTCAC 954
Db 661 TCAACTGTCCAGATATTTGATAATGGCAGCTTCTGTTCCAGTGGGACCATGTCAC 720
QY 955 CTGCAGGATATTAACAACCTGGAGCTTTCATTTCCAGGCCACACCTCTCATGGACGG 1014
Db 721 CTGCAGGATATTAACAACCTGGAGCTTTCATTTCCAGGCCACACCTCTCATGGACGG 780
QY 1015 CCATCATCTTTGGATACAAGAAATCCCTGTCCTGTCACACAGATAAGTTCACCAAC 1074
Db 781 CCATCATCTTTGGATACAAGAAATCCCTGTCCTGTCACACAGATAAGTTCACCAAC 840
QY 1075 CATCCAGTGAAGTCCGGTGTGTCATGCTGTCGTGGTCCAGGATCCAGCAATA 1134
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QY 1135 CCATGTTTCGAAGAACAAATTTATGAATATCCAGTAGAAGTACAAATGTCACAA 1194
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QY 1255 TGTGGCCCTTGTGTCCTCCAGATTTGTTTCAACTGCAAGTGTGGTCCAGCAAACTTCAA 1314
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QY 1309 CTTCAAGATGCTCCAGTGGATTTGATCGCCATCGCAGTGGTGGTGGACAGTGGATGC 1368
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QY 1486 AGGAGAGCTGTGACATCTCAGATGCTTACAGCTGCTTACAGAGATGACAGAGATA 1545
Db 1865 AGAAGAGCAGTGAATCTCAGTTTCCACAGCTCCCTACAGAGATGATACCAAGATA 1924
QY 1546 GCCCTACATCTCAAGACAGTGGAGCTCCACAGATGACAGTGCAGCTGAGAGAAAGGA 1605
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QY 1606 GGAACCTCCATGACAGCTCATTTGTTGGAAATCTCATCTTGTCTCATTTATAGCAGG 1665
Db 1985 GGAACCTCCACAGCTGCTCATTTGGAATCTCATCTGCTGCTCATTTGTTAGCCACA 2044
QY 1666 GCCATCTGGTCAGTGTATGTATCATCCATCCACATCAGCAGCCAGCATCTCTTC 1725
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Db 2225 TAAATTTTCTAGGACAGACAAACACCACTAGTACTGGTTTACAGGTTTAAAGACTAAATTTT 2284

QY 1905 GCTTATGCTATTAGACAAACACACACACACACACACACACACACACACACACACAC 1964
Db 2285 GCCTATACCTTTAGACAAACAAACAAACA-----CACACACAAACAGCTCTTAG 2335
QY 1965 CTGCTGTAGACAGAGGCGACGAGATTCTTGACAAGCCCGCCAGCCAGG-----AACATT 2019
Db 2336 CTGCTGTAGGCTGAA-GAAGACAGAGATTCTTGACAAGCTCAGCCCGAGAAACAAAGGT 2394
QY 2020 GAAGAGAAACTCAGACTTGTGTACAGACACCACTGATCAATGATTAAGAAATTCCTTAGTG 2079
Db 2395 AAACAAAAACTAAACTTATACAGATACCAATTTACTGTACATAGAAATTCCTTAGTG 2454
QY 2080 GAATGACATCCATGGTTTCAAGAGAACATCTCCGGTGGACTTCCAGGAGTGTGACAGAGA 2139
Db 2455 GAATGTCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAAGTATGACAAGA 2514
QY 2140 TGACGATGCTTTGGTTTAGGTGCAGGGTTGCAA 2174
Db 2515 TTATATGCTTTGGCTTAGGTGCAGGGTTGCAA 2549

RESULT 5

AAH23066
ID AAH23066 standard; cDNA; 3095 BP.

XX AAH23066;

AC AC
XX XX
DT 17-SEP-2001 (first entry)

XX Stem cell growth factor-like polypeptide encoding cDNA.

XX Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
KW degenerative disease; Alzheimer's disease; nutritional supplement;
KW cytosolic; neurotrophic; neuroprotective; hemostatic; antisense-therapy;
KW gene-therapy; cell proliferation; stem cell growth factor; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 123..1712

FT /*tag= a

XX WO200153500-A1.

XX 26-JUL-2001.

XX 23-DEC-2000; 2000WO-US35260.

XX 21-JAN-2000; 2000US-0488725.

PR 07-APR-2000; 2000US-0545714.

PR 11-APR-2000; 2000US-0547358.

XX (HYSE-) HYSEQ INC.

XX Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;

PI Chao C;

XX WPI; 2001-451909/48.

DR P-PSDB; AAB85394.

XX Isolated polypeptide with stem cell growth factor-like activity for

PT treatment of leukemia, hemophilia, and degenerative diseases like

PT Alzheimer's disease and to generate new tissues and organs -

XX Claim 1; Page 134-137; 154pp; English.

XX The invention provides novel human stem cell growth factor-like

CC polypeptides and polynucleotides encoding them. The polypeptides having

CC stem cell growth factor-like activity, can be expressed by standard

CC recombinant methodology. The polynucleotides and polypeptides can be

CC used to induce differentiation of embryonic and adult stem cells to give

CC rise to different cell types. They may also be used in the treatment of

CC leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
CC They may also be utilized to generate new tissues and organs that may aid
CC patients in need of transplants. They can also be used as nutritional
CC supplements. The present sequence represents a stem cell growth factor-
CC like polypeptide encoding cDNA.
xx
SQ

Sequence 3095 BP; 950 A; 687 C; 654 G; 804 T; 0 other;
Query Match 66.2%; Score 1440.4; DB 22; Length 3095;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1700; Conservative 0; Mismatches 291; Indels 25; Gaps 6;

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DB 95 GCTGGGGTAGGAGGTGGCGGCGGCGCATGGGAGGTTCCGAAAGCGCGACCTGGCGCG 154
QY 288 AGCAGGAGTTATGTTACTTTGTCACHTTTTACAGACCGGTTTCCAGTTTCGCCCGCGGA 347
DB 155 TGCAGGAGTTATGTTACTTTGTCACHTTTTCCAGGACCGGTTTCCAGTTTCGCCCGGA 214
QY 348 GCTGCGACCATACCAATGATTGGATTATGAAGTTACAAACGCTTTTCTTGGGAATGA 407
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QY 408 AGAGGGGTAGAGTGGACTCTCAAGCATACACACAGGTCGAAAGAAATTTGGACCC 467
DB 275 GGAGGAGGTGGAAGTTGATTACACGCGTACAGCCAGGTCGAAAGAAATTTGGACTT 334
QY 468 TTTTAAGGAGTAGACACAAACAGACCCAGTGGCCAGGCTCTCCAGAGTCCCAAGG 527
DB 335 TCTCAGGCGGTAGACACGACCGAGCAAGCGTGGCCAGGCTCTCTGAGCCCGAGAAG 394
QY 528 GTTCACTGACCTGCTACTGGATGAGGACAGGACAAATACACCCAGATAGAGGAGGAC 587
DB 395 CTTCACAGACCTGCTGCTGATGATGGCAGGACAAATACACTCAGATCGAGGAGGATAC 454
QY 588 GGATCAATTAATCACTTCTCGGATATATGTCAGGGATCTCGCCAGCGGGATCT 647
DB 455 AGACCAATTAATCACTTCTCGGATATATGTCAGGCTCTGATCTGCGCCGGGATTT 514
QY 648 GTGGGTTAAATAGACCAATGGAAGAACAAAGTGAAGATTCACGGGATCTTTCCAA 707
DB 515 ATGGGTGAACATAGACCAATGGAAGAACAAATGAAGTGAAGATTCATGGAATTTGCCA 574
QY 708 CACTCATCGCAAGCTGCAAGAGTGAATCTGCTTCGATTTTCATTTTATGGTCAATTT 767
DB 575 TACTCATCGCAAGCTGCAAGAGTGAATCTGCTTCGATTTTCATTTTATGGCCACTT 634
QY 768 TCTAAATGAAGTCACTGTGGCAACTGGGGTTTTCATATATATCTGAGAAAGTTGTACATCG 827
DB 635 CTTACGTGAATCACTGTGGCAACCGGGGTTTCATATACACTGGAGAGTCTGATACCG 694
QY 828 AATGCTCAGAGTACACAGTATATAGCTCCTTTTATGGCAATTTTATCCAGTGTATC 887
DB 695 AATGCTAACAGCCACACAGTATAGTACCTTTTATGGCAATTTTATCCAGTGTATC 754
QY 888 CAGAAATTAACATGTCAGATATTTGATATGTCAGAGCTCTGTTGTCAGTGGGACCA 947
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QY 1008 GGACGGCGCATCATCTTTGGATACAAAGAAATTCCTGCTGTCGTCACAGATAAGTTC 1067
DB 875 GGATGACGGAATCATCTTTGGATACAAAGAAATTCCTGCTGTCGTCACAGATAAGTTC 934
QY 1068 TACCAACCATCCAGTAGCGGGTGTCTGATGCAATTTGTCGGTCCACAGGATCCA 1127

DB 935 AACCAATCATCCAGTGAAGAGTGGACTGTCGATGCAATTTGCTGTGTCACAGATCCA 994
QY 1128 GCAATPACCCAAATGTTGGAAGAAAGAACAAATTTATGAATATACCCAGTAGAACATCAAA 1187
DB 995 ACAATTTCCCAATGTTGGAAGAAAGAACAAATTTATGAATACCAACCCAGTAGAGCTACAA 1054
QY 1188 GTCCAAATTTACCAACATCTCAGCTGTGGAGATGACTCCACTTCCACATGCTCTCCAGTT 1247
DB 1055 GTCAAAATTTACCAACATTTCCGCTGTGGAGATGACCCCATTTACCCACATGCTCTCCAGTT 1114
QY 1248 CAATGTTTGTGGCCCTTGTGTCTCTCCAGATTTGTTTCACTCAGTTTGGTTCAGCAA 1307
DB 1115 TAACAGATGTGGCCCTGTGTATCTCTCAGATTTGCTCAGATTTGCTCAGTGTGGTAGTAA 1174
QY 1308 ACTTCAAGATGCTCCAGTGGATTTGATCGCATCGCAGGACTGGGTGGAGCTGGAGT 1367
DB 1175 ACTTCAAGATGTTCCAGTGGATTTGATCGCTCTCGCAGGACTGGGTGGAGCTGGAGT 1234
QY 1368 CCGGAGAGGTACAGTCAAAAGAGAGATGTGTGAGAGACAGAGCCAGGAGAGA---C 1424
DB 1235 CCTGAAG-----AGTCAAAAGAGAGATGTGTGAGAATACAGAACCCAGTGGAACTTC 1288
QY 1425 ATCTCAAACTACACAGACCTCCACACAGACCACTCAATTCAGGCTCCTGACCCAC 1484
DB 1289 TTCTCGAACCCACCAACCATAGGAGGACACACCCAGTTTCAAGGTCCTTAATACCC 1348
QY 1485 CAGGAGAGTGTGACATCTCAGATGCTTACAGGCTGCTTACAGAGATGACAGAGAT 1544
DB 1349 CAGAGAGAGTGTGACTCTCAGTTTCCACAGGCTCCTCTACAGAGATGATACCAAGAT 1408
QY 1545 AGCCCTACATCTCAAAAGACAGTGGAGCTTCCACAGATGACAGTGCAGTGCAGTGAAGAAAG 1604
DB 1409 AGCCTACATCTAAAGATTAATGGAGCTTTCAGATGACAGTGCAGTGCAGTGAAGAAAG 1468
QY 1605 AGAACCCCTCCATGAGGCTCATTTGTTGAATCTCATTTGTTGCTCATTATAGCAGC 1664
DB 1469 GGAACCCCTCCAGCTGGCTCATGTTGGAATCTCATCTGTTGCTCATTGTAGCCAC 1528
QY 1665 GGCATCTCTGTCAGAGTGTATATGATCACCATCCACATCAGCAGCAGCAGCTCTCT 1724
DB 1529 AGCATCTCTGTCAGAGTGTATGATCACCCACCATCAGTGCAGTGCAGTGCAGTCTCT 1588
QY 1725 CATTGAGAGACGCCCAAGCAGATGGCCAGCAATTAAGTTTGAAGAGGCTCAGACACCC 1784
DB 1589 TATTGAGAGACGCCCAAGCAGATGGCTTGCATGAATTTAGAAGAGGCTCTGGACATCC 1648
QY 1785 TGCTATGAGAGATTTGAACAGTTGGAGAGAAAGAGTTTATTTATCAGAGCAGTG 1844
DB 1649 TGCTATGCTGAAGTTGAACAGTTGGAGAGAAAGAGGCTTTATTGATCAGAGCAGTG 1708
QY 1845 CTAAATTTT-TAGGACAGAGCAGCAGTACTGCTTACAGGTTTGAAGCTTAAAGCTT 1903
DB 1709 CTAAATTTTCTAGGACAGAACACACAGTACTGTTTACAGGTTTGAAGCTTAAATTT 1768
QY 1904 TGCTTATGATTTTGAACAAACAGACACACACACCCACACACACAAAGAGGCGCTAA 1963
DB 1769 TGCTATACCTTTAAGACAAACAAACAAACA-----CACACAAACAAAGCTCTAA 1819
QY 1964 ACTGCTGTAGACAGAGGCGGAGAGATTTCTGGAACAGCCAGCCAGG-----AACAT 2018
DB 1820 GCTGCTGTAGCTGAA-GAAGACAGATTTCTGGACAGCTCAGCCAGGAAACAAAGG 1878
QY 2019 TGAAGAGAAACTCAGACTTTGACAGACACCATGTACAATGATTAAAGATTTCCCTAGT 2078
DB 1879 TAAACAAAAAACTAAAACTTATACAGATACCATTTACATTTACATGAACATAGAAATTCCTAGT 1938
QY 2079 GGAATCAGATCATGTTTCCAGAGGAACATCTCCGGTGGACTTGCAGAGTGTGACGAG 2138
DB 1939 GGAATCTCATCTATAGTTTCACTCGGAACATCTCCCGTGGACTTATCTGAATGATGACAG 1998
QY 2139 ATGACGATCTTTTGGTTTATGTTGAGGTTGCAAA 2174

[illegible]

427	QY	TCTCAGCATACACACAGGTGGAAAAGAAATGTGGACCCCTTTTAAGCCAGTAGACACA	486
181	Db	TCACACGGGTACAGCCACAGGTGAAAAGAAATCTTCTCAGCGCGGTAGACAGC	240
487	QY	AACAGAGCCAGCATCGGCGCAAGCCTCTCCAGAGTCCAAAAGGTTCACTGACCTGCTACTG	546
241	Db	AACCGAGCAACGCTCGGCGAAGACTCTCTGAGCCCCAGAAGCTTCACAGAGCTGCTGCTG	300
547	QY	GATGACGACAGGACAAATACACCCAGATAGAGGAGGACACAGCATACAAATTTACTTACATT	606
301	Db	GATGATGGCGAGGACAATACATCTCAGATCGAGGAGGATACAGACCCAAATTTACTATATA	360
607	QY	TCTCGGATATATGTTCCAGCGGATTTGCCAGCCGGGATCTGTGGTTAAACATAGACCAA	666
361	Db	TCTCCGAATATATGTTCCATCTGATCTGCCAGCGGGGATTTATGGGTGAACATAGACCAA	420
667	QY	ATGGAAAAGACAAGTGAAGATTACGGGGATACTTTCCAAACACTCATCGGCCAAGCTGCA	726
421	Db	ATGGAAAAGGATTAAGTGAAGATTCATGGAAATATTGTCANTACTCATCGGCCAAGCTGCA	480
727	QY	AGAGTGAATCTGTCCTTCGGATTTTCCATTTTATGGTCAATTTTCTTAATGAAGTCACTGTG	786
481	Db	AGAGTGAATCTGTCCTTCGGATTTTCCATTTTATGGCACTTCTCAGGTGAATCACTGTG	540

QY	1863	GCAGCACCGACTACTGGCTTACAGGTGTTTAAGACTAAAACTTTGGCTTATGCATTTAAGACA	1922		
Db	1615	ACAACACCGACTACTGGTTTACAGGTGTTTAAGACTAAAAATTTTGGCTTATGCATTTAAGACA	1674		
QY	1923	AACAGACACACAACCCACACACACACACACAAAGAGCCCTAAACCTGCTGTAGACAGAAAGGG	1982		
Db	1675	AACAACAACAACA-----CACACACAACAAGCTCTTAAGCTGCTGTAGCTGAA-GA	1724		
QY	1983	CGACGAGATTCTTGGCAAGCCCGACGCCAGG-----AACATTGAAAGAAACCTCAGACT	2037		
Db	1725	AGACAAGATTCTTGGCAAGCTCAGCCAGGAAACAAAGGGGTAAACAAAAAACTAAAAACT	1784		
QY	2038	TGTACAGACACCATGTACATAATGATTAAAGATNTCCCTAGTGGATGACATCCATGGTTC	2097		
Db	1785	TATCAAGATACCATTTTACACTGAACATAGAATTCCTAGTGGAAATGTCATCTATAGTTC	1844		
QY	2098	ACAAGGAAACATCTCCGGTGGACTTGCACGAGGTGTGACGAGATGACGATGCTTTTGGTTT	2157		
Db	1845	ACTCGAACATCTCCGGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTT	1904		
QY	2158	AGGTGCAGGGTTGCAAA	2174		
Db	1905	AGGTGCAGGGTTGCAAA	1921		
RESULT 8					
AAC87054					
XX	ID	AAC87054 standard; cDNA; 2557 BP.			
AC	AAC87054;				
XX	20-APR-2001	(first entry)			
DT	Nucleotide sequence of human polypeptide PRO6003.				
DE	Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;				
XX	PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;				
KW	PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;				
KW	PRO1600; PRO3940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;				
KW	PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;				
KW	PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;				
XX	ss.				
XX	Homo sapiens.				
OS					
XX	Key	Location/Qualifiers			
XX	CDS	601..2190			
FT	/*tag= a				
XX	WO2000077037-A2.				
XX	21-DEC-2000.				
XX	22-MAY-2000; 2000WO-US14042.				
XX	15-JUN-1999;	99US-0139695.			
PR	20-JUL-1999;	99US-0145070.			
PR	26-JUL-1999;	99US-0145698.			
PR	17-AUG-1999;	99US-0149396.			
PR	01-SEP-1999;	99WO-US20111.			
PR	08-SEP-1999;	99WO-US20594.			
PR	15-SEP-1999;	99WO-US21090.			
PR	15-SEP-1999;	99WO-US21547.			
PR	30-NOV-1999;	99WO-US28313.			
PR	01-DEC-1999;	99WO-US28301.			
PR	02-DEC-1999;	99WO-US28585.			
PR	07-DEC-1999;	99US-0169495.			
PR	05-JAN-2000;	2000WO-US00219.			
PR	18-FEB-2000;	2000WO-US04341.			
PR	18-FEB-2000;	2000WO-US04342.			
PR	22-FEB-2000;	2000WO-US04414.			
PR	01-MAR-2000;	2000WO-US05601.			
PR	02-MAR-2000;	2000WO-US05841.			

PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX (GETH) GENENTECH INC.
XX PA
XX PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
PI Pironi NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2001-050091/06.
DR P-PSDB; AAB31211.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
XX Claim 2; Fig 65; 244pp; English.
XX
XX The present sequence encodes a human secreted and transmembrane
XX polypeptide. The specification describes human polypeptides, designated
XX PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO286,
XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
XX PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
XX PRO337, PRO411, PRO356, PRO246, PRO265, PRO941, PRO1096, PRO6003,
XX PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
XX can be modulated with agents that bind to these polypeptides, resulting
XX in the death of the cells. The polynucleotides encoding these
XX polypeptides are useful in the recombinant production of the
XX polypeptides, as a hybridisation probe to screen libraries to isolate
XX homologous sequences, or to map the gene. They may also be used for
XX analysing genetic disorders, and to produce transgenic animals which are
XX useful for the development and screening of therapeutically useful
XX reagents. The polynucleotides can also be used in gene therapy e.g. to
XX replace a defective gene.
XX
XX Sequence 2557 BP; 718 A; 639 C; 615 G; 585 T; 0 other;
XX
Query Match 65.4%; Score 1423.4; DB 22; Length 2557;
Best Local Similarity 85.2%; Pred. No. 0;
Matches 1662; Conservative 0; Mismatches 264; Indels 25; Gaps 6;
QY 233 GGGAGAGAGTCCGGCAGCGCATGGCAAGTTCCTCGGAGGCGCCAGCTGGCCGACGAG 292
DB 578 GGGAGCGCCCGACCGCGGAAATGGCGAGGTTCGGAGGCGCCAGCTGGCCGCTGCGAG 637
QY 293 GAGTTATGTTACTTTGCTCACTTTTAAACAGACCGGTTCCAGTTCGCCCGCAGCGGAGCGCTG 352
DB 638 GAGTTATGTTACTTTGCCACTTCTTCAAGCGCCAGTTTCAGTTCCGCGATGGGAAACCGC 697
QY 353 GACACCATACCATGATTTGATTTATGAGTTTACAAAGCGTTTCCAGTTCGCCCGCAGCGAGG 412
DB 698 GAGACCAATTCCTTGATTTGGCAGTATGGAGTTTACTCAGCGCTTCCTCCACAGAGGAGG 757
QY 413 GGGTAGAAGTGGACTCTCAAGCATACAAACACAGGTGGAAAGAAATGTGGACCTTTTA 472
DB 758 AGTGGAGTGTGATTCACACCGGTACAGCCAGCCAGGTGGAAAGAAATGTGGACTTTCTCA 817
QY 473 AGCGAGTAGACAAACAGAGCCAGCATGGGCCAAGCGCTTCACAGAGTCCAAAGGGTTCA 532
DB 818 AGCGGCTAGACAGAACCGAGCAAGCGTGGCGAAGACTCTCTCTGAGCCCAAGAGCTTCA 877
QY 533 CTGACCTGTCTAGTATGAGGACAGGACAAATACACCCAGATCAGGAGGACAGCGATC 592
DB 878 CAGACTGTCTGTGATGATGGCGAGGACAAATACACTCAGATCAGGAGGATACAGACC 937
QY 593 ACAATTACTACATTTCTGGATATATGTTCCACCGGATCTTCCAGCGGGATCTGTGGG 652
DB 938 ACAATTACTATATCTCGAATATATGTTCCATCTGATTTCTGCCAGCGGATTTATGGG 997

QY 553 TTACATACACCAATGGAAAAAGAAAGTGAAGATTCACGGGATACATTTTCCAACTC 712
DB 998 TGAACATACACCAATGGAAAAAGAAAGTGAAGATTCATGGRATATTTGTCATCTC 1057
QY 713 ATCGCAAGCTGCAAGAGTGAATCTGCTCTCGATTTTCCATTTTATGTTGCTCATTTCTAA 772
DB 1058 ATCGCAAGCTGCAAGAGTGAATCTGCTCTCGATTTTCCATTTTATGTTGCTCATTTCTTAC 1117
QY 773 ATGAAGTCTACTGTGGCACTGGGGTTTCATATATCTGAGAGTGTGATGATGATGATGATG 832
DB 1118 GTGAATCTACTGTGGCACTGGGGTTTCATATACATCTGAGAGTGTGATGATGATGATGATG 1177
QY 833 TCACAGCTACACAGTATATAGTCTCTTAATGGCAAAATTTGATCCCACTGATCCAGAA 892
DB 1178 TACACCCACACAGTACATAGACACCTTTAATGGCAAAATTTGATCCCACTGATCCAGAA 1237
QY 893 ATTCAACTCTCAGATATTTTGTATATGTCACAGCTCTCTGTTGTTCCAGTGGGACATGTC 952
DB 1238 ATTCAACTCTCAGATATTTTGTATATGTCACAGCTCTCTGTTGTTCCAGTGGGACATGTC 1297
QY 953 ACCTGAGGATATTTACAACTGGGAAGCTTCCATATTCACAGCTCCAGCCACACTCTCATGAGC 1012
DB 1298 ATCTCAGATATTTATTAACCTGGGAGCTTCCATTTCCAGGCACTCTCATGATG 1357
QY 1013 GGGCATCATCTTTGGATACAAAGAAATCCCTGCTTGGTCACACAGATATGTTTACCA 1072
DB 1358 GACGAATCATCTTTGGATACAAAGAAATCCCTGCTTGGTCACACAGATATGTTTACCA 1417
QY 1073 ACCATCCAGTGAAGTGGGTTGCTGTGATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1132
DB 1418 ATCATCCAGTGAAGTGGGACTGTCGATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1477
QY 1133 TACCAATCTTGAAGAGAAACAAATTTATGATATATCCAGTGTAGATACAAATGTTCA 1192
DB 1478 TTCCCAATCTTGAAGAGAAACAAATTTATGATATATCCAGTGTAGATACAAATGTTCA 1537
QY 1193 AAATTACCAATCTCAGCTGTTGGAGTACATCCACTTCCACATGTTCCAGTGTCAATG 1252
DB 1538 AAATTACCAATCTCAGCTGTTGGAGTACATCCACTTCCACATGTTCCAGTGTCAATG 1597
QY 1253 GTTGTGGCCTTGTGTTGCTCTCGAGATGTTTCACTGAGTGTGGTGCACAACTTC 1312
DB 1598 GATGTGGCCTTGTGTTGCTCTCGAGATGTTTCACTGAGTGTGGTGCACAACTTC 1657
QY 1313 AAAGATGTTCCAGTGTGATTTGATTCGCTGCGAGACTGGTGGACAGTGGATGCTGCTG 1372
DB 1658 AAAGATGTTCCAGTGTGATTTGATTCGCTGCGAGACTGGTGGACAGTGGATGCTGCTG 1717
QY 1373 AAGAGTGTACGTCACAAAGAGAAAGTGTGTGAGAGACAGAGCCAGGAGAGA ---CATCTC 1429
DB 1718 AAG-----AGTCAAAAGAGAAAGTGTGTGAGAAATACAGAACAGTGGAACTTCTTCTC 1771
QY 1430 AAATACACAGACCTCCACAGACACCATTCATTCATTTGAGGTTCTGACCCACCCAGGA 1489
DB 1772 GAACCAACCAACCGTAGGAGCGCAACCCAGCTTCAGGGTCTCTAACTACCCAGAA 1831
QY 1490 GAGCTGTGATCTCTCAGATGCTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
DB 1832 GAGCACTGACTTCTCAGTTTCCACAGCTCTCCCTTACAGAGATGATACCAAGATAGCAC 1891
QY 1550 TACATCTCAAGAGAGTGGAGCTCCACAGATGACAGTGTGAGAGTGTGAGAGAGAGAGAA 1609
DB 1892 TACATCTCAAGAGATATGAGCTTCTACAGATGACAGTGTGAGAGTGTGAGAGAGAGAGAA 1951
QY 1610 CCTCCATCAGCGCTCATTTGTTGGAATTTCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1669
DB 1952 CCTCCATCAGCGCTCATTTGGAATTTCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2011
QY 1670 TTGTGTGACAGTGTATATGATACCAATCCAAATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1729
DB 2012 TTCTTGTGACAGTGTATATGATACCAATCCAAATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2071
QY 1730 AGNAGCGCCCAAGAGAGTGGCCAGCAATGAAGTTTCGAGAGGCTCAGGACACCCCTGCT 1789

QY 1036 GAAATCCCTGTTGGTCCACAGATAAGTTCTTACCAACCATCCAGTGAAGTGGGTTG 1095
DB 781 GAAATCCCTGTTGGTCCACAGATAAGTTCTTACCAACCATCCAGTGAAGTGGGTTG 840
QY 1096 TCTGATGCAATTTCTGTTGGTCCACAGATAAGTTCTTACCAACCATCCAGTGAAGTGGGTTG 1155
DB 841 TCGATGCAATTTCTGTTGGTCCACAGATAAGTTCTTACCAACCATCCAGTGAAGTGGGTTG 900
QY 1156 ATTATGAATATACCGAGTAGTAACATCAAAATGTCCAAATTTACCAACATCTCAGCTGTG 1215
DB 901 ATTATGAATATACCGAGTAGTAACATCAAAATGTCCAAATTTACCAACATCTCAGCTGTG 960
QY 1216 GAGATGACTCCATCTCCACATGTTCCAGTTCATAGTTGTGGCCCTGTGTGTCCTCG 1275
DB 961 GAGATGACTCCATCTCCACATGTTCCAGTTCATAGTTGTGGCCCTGTGTGTCCTCG 1020
QY 1276 CAGATTTGGTTTCAACTGCACTTGGTCCAGCAAACTTCAAAAGATGTCCTCAGTGGATTTGAT 1335
DB 1021 CAGATTTGGTTTCAACTGCACTTGGTCCAGCAAACTTCAAAAGATGTCCTCAGTGGATTTGAT 1080
QY 1336 CGCATCGGAGACAGTGGTGGACATGATGCCGGAGAGAGTACAGTCAAAAGAGAG 1395
DB 1081 CGTATCGGAGACAGTGGTGGACATGATGCCGGAGAGAGTACAGTCAAAAGAGAG 1134
QY 1396 ATGTGTGAGAGACAGAGCCAGGAGAGA---CATCTCAAACTTACCAGCACCCTCCACACG 1452
DB 1135 ATGTGTGAGATACAGAACCATGTTGAACTTCTCTCGAACCCACACACATAGGAGG 1194
QY 1453 ACCACATGCAATTCAGGTCCTGACACACAGAGAGTGTGACATCTCAAGATGCGT 1512
DB 1195 ACACCCAGCATTCAGGTCCTTAACTACACAGAGAGTGTGACATCTCAAGATGCGT 1254
QY 1513 ACCAGCTCGCTACAGAGATGACAGAGATAGGCTTACATCTCAAAAGACAGTGGAGCC 1572
DB 1255 ACCAGCTCGCTACAGAGATGACAGAGATAGGCTTACATCTCAAAAGATAGGAGCT 1314
QY 1573 TCCAGATGACAGTGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632
DB 1315 TCTACATGACAGTGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1374
QY 1633 GGAATTCATCTGTTGCTTCATTATAGCAGGCGCCATCTGTTGACAGTGTATATGAT 1692
DB 1375 GGAATTCATCTGTTGCTTCATTATAGCAGGCGCCATCTGTTGACAGTGTATATGAT 1434
QY 1693 CACATCCACATCAGAGCAGCATCTTCTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1752
DB 1435 CACACCCACATCAGAGCAGCATCTTCTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1494
QY 1753 GCAATGAATTTGAGAGAGCTCAGGACAGCCTGCTGCTATGAGAGAGTGAACAGTGGGA 1812
DB 1495 GCGATGAGTTTGAAGAGAGCTCTGGACATCTGCTATGCTGAGAGTGAACAGTGGGA 1554
QY 1813 GAGAAAGAGTTTATTTATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1848
DB 1555 GAGAAAGAGCTTTATTTATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

RESULT 10
AAI60009/c
ID AAI60009 standard; cDNA; 2668 BP.
XX
AC
AAI60009;
XX
DT 22-OCT-2001 (first entry)
DE Human polynucleotide SEQ ID NO 3998.
XX
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

leukaemia; ss.
Homo sapiens.
WO200153312-A1.
26-JUL-2001.
26-DEC-2000; 2000WO-US34263.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Pang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
P-PSDB; AAM40853.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Claim 1; SEQ ID NO 3998; 10078pp; English.
The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nontropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
specification.
XX Sequence 2668 BP; 721 A; 517 C; 579 G; 851 T; 0 other;
SQ
Query Match 54.9%; Score 1195.2; DB 22; Length 2668;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 183; Indels 25; Gaps 6;
QY 586 ACGATCACAATTACTACATTTCTCGATATATGTTCCAGCGGATTCGCCAGCGGGAT 645
DB 2643 ACAGACCACAATTACTATATATCTCGATATATGTTCCATCTGATCTGCCAGCGGGAT 2584
QY 646 CTGTGGTTAAACATAGACCAATGGAAGAAAGACAAAGTGAAGATTCACGCGGATATCTCC 705
DB 2583 TTATGGTGAACATAGACCAATGGAAGAAAGATGAAGTGAAGATTCATGGAATTTGTC 2524
QY 706 AACACTCATCGCAAGCTGCAAGATGATCTGCTCTGATTTTCCATTTTATGTCAT 765
DB 2523 AATCTCATCGCAAGCTGCAAGATGATCTGCTCTGATTTTCCATTTTATGTCAT 2464
QY 766 TTTCTAAATGAAGTCACTGTGGCACTGGGGTTCATATATATCTGAGAGAGTGTACAT 825
DB 2463 TTCTACGTGAATCACTGTGGCACTGGGGTTCATATATCTGAGAGAGTGTACAT 2404
QY 826 CGATGCTCACACTACAGTATATAGTCTCTTAAATGGCAATTTTCATCCAGTCTA 885

1329	TTTGCCTATACCTTTTAAGACAAACAAACA-----CACACAAACAGCTCT	127
1962	AAACTGCTGTAGACAAAGGGGAGAGATTTCTTGCAAGCCAGCCAGG-----AAC	2016
1278	AGCTGCTGTAGCCTGAA- GAAGACAAGATTTCTTGCAAGCTCAGCCAGGAACAAG	1220
2017	ATTGAAGAGAAACTCAGACTTGTACACACACACCATGTACATGATTAAAGAATTCCTTA	2076
1219	GGTAACACAAAAAACTAAAACTTATACAGATACCATTTACACTGAACATAGATTCCCTA	1160
2077	GTGGAATGACATCCATGGTTCCACAAGGAACATCTCCGGTGGACTTGCAGGAGTGTACG	2136
1159	GTGGAATGCTATCTATAGTTCACCTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACA	1100
2137	AGATGACAGCTTTTGGTTTATAGTGCAGGGTGCAAA	2174
1099	AGATTATAATGCTTTTGGCTTAGTGCAGGGTGCAAA	1062
RESULT 11		
AAI60010/c		
AAI60010 standard; cDNA; 2668 BP.		
XX	AAI60010;	
XX	22-OCT-2001 (first entry)	
XX	Human polynucleotide SEQ ID NO 3999.	
DE	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;	
DE	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukaemia; ss.	
XX	Homo sapiens.	
XX	WO200153312-AL.	
XX	26-JUL-2001.	
XX	26-DEC-2000; 2000WO-US34263.	
XX	21-JAN-2000; 2000US-0488725.	
XX	25-APR-2000; 2000US-0552317.	
XX	09-JUL-2000; 2000US-0598042.	
XX	19-JUL-2000; 2000US-0620312.	
XX	03-AUG-2000; 2000US-0653450.	
XX	14-SEP-2000; 2000US-0662191.	
XX	19-OCT-2000; 2000US-0693036.	
XX	29-NOV-2000; 2000US-0727344.	
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
XX	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
XX	Zhao QA, Zhou P, Goodrich R, Drmanac RT;	
XX	WPI; 2001-442253/47.	
XX	P-PSDB; AAM40854.	
XX	Novel nucleic acids and polypeptides, useful for treating disorders	
XX	such as central nervous system injuries -	
XX	Claim 1; SEQ ID NO 3999; 10078pp; English.	
XX	The invention relates to human nucleic acids (AAI57798-AAI61369) and	
XX	the encoded polypeptides (AAM38642-AAM42213) with nootropic,	
XX	immunosuppressant and cytostatic activity. The polynucleotides are useful	
XX	in gene therapy. A composition containing a polypeptide or polynucleotide	
XX	of the invention may be used to treat diseases of the peripheral nervous	
XX	system, such as peripheral nervous injuries, peripheral neuropathy and	

FT which alters the reading frame"
FT /transl_except- (pos:879..884,aa:Pro)
FT /transl_except- (pos:909..914,aa:Ser)
FT /transl_except- (pos:927..928,aa:Asp)
FT /note= "This codon has an apparent 1 nucleotide deletion
FT which alters the reading frame"
FT /product= "human protein SEQ ID NO 2"
FT /partial
FT /note= "CDS lacks an initiation codon"
XX
XX WO200152616-A2.
XX
XX
PD 26-JUL-2001.
XX
XX
PF 22-DEC-2000; 2000WO-US35190.
XX
XX
PR 23-DEC-1999; 990S-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-451890/48.
XX P-PSDB; AAG64527.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 1; Page 15; 135pp; English.
XX
XX The invention relates to an isolated human polynucleotide (AAH75398)
XX encoding a novel polypeptide (AAG64527) useful in antisense-therapy and
XX gene-therapy, in diagnostics, forensics, gene mapping and identification
XX of mutations, responsible for genetic disorders and other traits.
XX Polynucleotide sequences with potential homology were also identified
XX (AAH93283-AAH93356).
XX
XX Sequence 2668 BP; 851 A; 579 C; 517 G; 721 T; 0 other;
Query Match 54.9%; Score 1195.2; DB 22; Length 2668;
Best Local Similarity 87.08; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 183; Indels 25; Gaps 6;
QY 586 ACGGATCACAATTTACTATCTTCGGATATATGTGCCAGCGGATTCGCCAGCGGGAT 645
DB 26 ACAGACACAATTTACTATATCTCGAATATATGTGCCATCTGATTCGCCAGCGGGAT 85
QY 646 CTGTGGTTAACTACACCAATGGAAAGACAAAGTGAAGATTCAGGATTTCC 705
DB 86 TTATGGGTGAACATGACCAATGGAAAGATGAAAGTGAAGATTCAGGATTTGTC 145
QY 706 AACACTCATCGGCAAGCTGCAAGAGTGAATCTGCTTCGATTTTCCATTTTATGTGTCAT 765
DB 146 AATACTCATCGGCAAGCTGCAAGAGTGAATCTGCTTCGATTTTCCATTTTATGCGCCAC 205
QY 766 TTCTTAATGAAGTCTACTGTGGCACTGGGGTTTCATATATACGTGGAGAGTTGTACAT 825
DB 206 TTCTTACGTGAATCTACTGTGGCACTGGGGTTTCATATACGTGGAGAGTGTGATCAT 265
QY 826 CGAATGCTACAGCTACAGATATATAGCTCTTAAATGGCAAAATTTGATCCCACTGTA 885
DB 266 CGAATGCTACAGCTACAGATATATAGCTCTTAAATGGCAAAATTTGATCCCACTGTA 325
QY 886 TCCAGAAATTCAGCTGTAGATATTTTGTATATGGCAGAGCTCTTGTGTCCAGTGGAC 945
DB 326 TCCAGAAATTCAGCTGTAGATATTTTGTATATGGCAGAGCTCTTGTGTCCAGTGGAC 385
QY 946 CATGTCCACCTCAGGATATTTACACCTGGGAAGCTTCACATTCAGGCCACACTCCTC 1005
DB 386 CATGTACATCTCCAGGATATTTAACTTGGGAAGCTTCACATTCAGGCCACACTCCTC 445

QY 1005 ATGGACGGCGGCATCATCTTTGGATACAAAGAAATCCCTGCTGTGGTCACACAGATAGT 1065
DB 446 ATGGATGGACGAATCATCTTTGGATACAAAGAAATTCCTGCTTTGGTCACACAGATAGT 505
QY 1066 TCTACCAACATCCAGTGAAGTGGGTGCTGCTGATGATTTGCGTGGTCCACAGGATC 1125
DB 506 TCAACCAATCATCCAGTGAAGTGGGTGCTGCTGATGATTTGCGTGGTCCACAGGATC 565
QY 1126 CAGCAAAATACCAATGTTGGAAGAAAGAAATTTATGAATATCACCGAGTAGACTCAA 1185
DB 566 CAACAAATTTCCCAATGTTGGAAGAAAGAAATTTATGAATATCACCGAGTAGACTCAA 625
QY 1186 ATGTCCAAAATTTACCAATCTCAGCTGTGGAGATGACTCCACTTCCACATGTCTCCAG 1245
DB 626 ATGTCAAAATTTACCAATCTCAGCTGTGGAGATGACTCCACTTCCACATGTCTCCAG 685
QY 1246 TTCAATGGTGTGGCCCTTGTGCTGCGAGATTTGTTCAACTGCGATTTGTTGCGAGC 1305
DB 686 TTTAACAGATGTGGCCCTTGTGCTGCGAGATTTGTTCAACTGCGATTTGTTGCGAGC 745
QY 1306 AAACCTTCAAGATGCTCCAGTGGATTTGATGCCATCGGAGGACTGGGTGGACAGTGA 1365
DB 746 AAACCTTCAAGATGCTCCAGTGGATTTGATGCCATCGGAGGACTGGGTGGACAGTGA 805
QY 1366 TGCCCGGAAGAGGTACAGTCAAAAGAGAGATTTGTGAGAGACAGAGCCAGGAGAGACA 1425
DB 806 TGCCCTGTAAG-----AGTCAAAAGAGAGATTTGTGAGATACAGAAACCAAGTGA 859
QY 1426 ---TCTCAAAATACCAAGACTCCACAGGACCCATGCAATTCAGGCTCCTGACACC 1482
DB 860 TCTCTCGAACCACCAACCAATAGAGCGCAACCCAGTTCAGGCTCCTAATACC 919
QY 1483 ACCAGAGAGCTGTGACATCTCAGATGCTTACAGGCTGCCCTACAGAGATGACACAGAG 1542
DB 920 ACCAGAGAGAGCTGTGACATCTCAGATGCTTACAGGCTGCCCTACAGAGATGACACAG 979
QY 1543 ATAGCCCTACATCTCAAGACAGTGGAGCTCCACAGATGACAGTGCAGCTGAGAGAAA 1602
DB 980 ATAGCCTACATCTCAAGATGAGGCTTCTACAGATGACAGTGCAGCTGAGAGAAA 1039
QY 1603 GGAGGAACCTCCATCAGGCTCATTTGTGGAATTTCTCATTTGGTCTCTATTATAGCA 1662
DB 1040 GGAGGAACCTCCACGCTGCCCTCATCTGCTGCTCATCTCTGCTCTCATTTAGCC 1099
QY 1663 GCGGCCATCTCTGTCAGCTGTATGTATCACCATCCACATCAGCAGCAGCATCTTC 1722
DB 1100 ACAGCCATCTTGTGACAGTCTATGTATCACCACCAACATCAGCAGCAGCATCTTC 1159
QY 1723 TTCATTTGAGAGCGCCCAAGCAGATGGCCAGCAATGAAGTTTCGAAGAGGCTTCAGGAC 1782
DB 1160 TTTATTTGAGAGCGCCCAAGCAGATGGCTCGGATGAAGTTTGAAGAGGCTCTGGACAT 1219
QY 1783 CTTGCCCTATGCAAGTTGAACAGTTGGAGAGAAAGAGGTTTTATTGTATCAGAGCAG 1842
DB 1220 CTTGCCCTATGCTGAAGTTGAACAGTTGGAGAGAAAGAGGTTTTATTGTATCAGAGCAG 1279
QY 1843 TGTAAATTT-TAGCAGCAGCAGCAGCAGTGGCTTACAGGTTTAAGACTTAAAC 1901
DB 1280 TGTAAATTTTAGCAGCAGCAGCAGCAGTGGCTTACAGGTTTAAGACTTAAAC 1339
QY 1902 TTTGCTTATGCTTTAAGCAAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1961
DB 1340 TTTGCTTATGCTTTAAGCAAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1390
QY 1962 AAATGCTGTAGACAGAGGCGCCAGGATTTCTGGACAAGCCAGCCAGCCAGG-----AAC 2016
DB 1391 AAGCTGCTGTAGGCTGAA-GAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAG 1449
QY 2017 ATTGAAGGAAACTCAGACTTGTACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2076
DB 1450 GGTAAACAAAACCTAAACCTTATACAAGATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1509
QY 2077 GTGGAATGACATCCATGGTTTCACAGGAACATCTCCGGTGGACTCCAGGAGGTGTGAGC 2136

Db	26	ACAGACCACAATTACTATATATCTCGAATATATGTGCTCCATCTGATCTGGCAGCCGGGAT	85
QY	646	CTGTGGGTAACTATAGACCAAATGGAAAAAGACAAGTGAAGATTACGGGATACTTTCC	705
Db	86	TTATGGGTGAACATAGACCAAATGGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCC	145
QY	706	RACACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCATTTTATGGTCAT	765
Db	146	RAATCTCAITCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCCATTTTATGGCCAC	205
QY	766	TTTCTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTTGGAGAAGTTGTACAT	825
Db	206	TTCTCTACGTGAATCACTGTGGCAACCGGGGTTTCATATACACTGGAGAAGTCGTACAT	265
QY	826	CGAATGCTCAGCTACACAGTATATAGTCTCCTTTAATGGCAAAATTTTGATCCCAAGTGA	885
Db	266	CGAATGCTACAGCCACACAGTACATAGCACCTTTAATGGCAAAATTCGATCCCAAGTGA	325
QY	886	TCCGAATAATCAACTGTCAGATATTTTGATAATGCGACAGCTCTGTGTGCCATGGGAC	945
Db	326	TCCGAATAATCAACTGTCAGATATTTTGATAATGCGACAGCACTTGTGTCCATGGGAC	385
QY	946	CATGTCCACCTGTCAGGATAATTACAACCTGGGAAGCTTCACATTCACAGCCACACTCCTC	1005
Db	386	CATGTACATCTCAGGATAATTATACCTTGGGAGCTTCACATCCAGGCAACCTGCTC	445
QY	1006	ATGAGCGGGCGCATCATCTTTTGGATACAAGAAATCCCTGCTGTGGTCCACAGATAAGT	1065
Db	446	ATGGATGAGCAATCATCTTTTGGATACAAGAAATCCCTGCTGTGGTCCACAGATAAGT	505
QY	1066	TCTACCAACCATCCAGTGAAGTTCGGTGTCTGTGATGCAATTTGTCGTGTCACAGGATC	1125
Db	506	TCACCAATCATCCAGTGAAGTCGGACTGTCGATGCAATTTGTGCTGTCCACAGGATC	565
QY	1126	CAGCAATACCCATGTTCCGAAGAAGACAATTTATGAATATACCCGAGTAGACTACAA	1185
Db	566	CAACAATTTCCCAATGTTCCGAAGAAGACAATTTATGAATACACCGAGTAGACTACAA	625
QY	1186	ATGTCCAAATTTACCAACATCTCAGCTGTGGAGATGACTCCACTTCCCACATGTCTCCAG	1245
Db	626	ATGTCAAAATTTAGCAACATTTCCGCTGTGGAGATGACCCCATTTACCCACATGCTCCAG	685
QY	1246	TTCAATGTTGTGGCCCTCTGTGTCCTCGCAGATTTGTTTCACTGCAGTTGTGTGAGC	1305
Db	686	TTTACAGATGTGGCCCTGTGATCTTCTCAGATGGCTTCACCTGCAGTTGTGTGAGT	745
QY	1306	AAACTTCAAGAGTCTCCAGTGGATTGATGCCCATCGCGAGGACTGGGTGGACAGTGA	1365
Db	746	AAACTTCAAGAGTCTCCAGTGGATTGATCGTCATCGCGAGGACTGGGTGGACAGTGA	805
QY	1366	TGSCGGGAAGAGTACAGTCAAAGAGAAGATGTTGTGAGAAGACAGAGCCAGAGAGACA	1425
Db	806	TGCCCTGAAG-----AGTCAAAGAGAGAGATGTTGTGAGATACAGAACCACTGGAAGCT	859
QY	1426	---TCTCAAACTACCAAGCCTCCCAACAGCAACCATGCAATTCAGGGTCCCTGACCAC	1482
Db	860	TCTTCTCGAACCAACCAACCATAGAGGGGCAACACCCAGTTTCAGGGTCCCTTAATACC	919
QY	1483	ACCAAGAGAGTGTGACATCTCAGATGTCCTACAGCCTGCCTTACAGAAGATGACACGAAG	1542
Db	920	ACCAAGAGAGTGTGACTTCTCAGTTTCCACAGCCTCCCTACAGAAGATGATCCAG	979
QY	1543	ATAGCCCTTACATCTCAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAGAA	1602
Db	980	ATAGCACTTACATCTCAAGAGATAATGGAGCTTCTACAGATGACAGTGCAGCTGAGAAGAA	1039
QY	1603	GGAGGAACCTTCCATGCAGAGCCCTCATTTGTTGGAATTTCTCATCTTGGTCTCATATAGCA	1662
Db	1040	GGGGGAACCTTCCAGCTGBCCTCATCTGTGGATTCCTCATCTTGGTCTCATTTGATGCC	1099
QY	1663	GGGGCCATCTGTGTGACAGTGTATATGTATACCACTCCAAACATCAGCAGCCAGCATCTTC	1722
Db	1100	ACAGCCATCTCTGTGACAGTCTATATGTATCACCAACCAACATCAGCAGCAGCATCTTC	1159

QY	229	GCAGGGGAGAGAGTCCGGGAGCGGCATGGCAAGTTCCGGAGGGCCGACCTGGCCGCA	288
Db	743	GTGGGGTAGGGAGGTGGGGGGGGGATGGGAGGTTCCCGAAGGGCCGACCTGGCCGCT	802
QY	289	GCAGGAGTTATCTTACTTTTACACAGACCGGTTCCAGTTCCGGCCACCGGGAG	348
Db	803	GCAGGAGTTATCTTACTTTTACACAGACCGGTTCCAGTTCCGGCCACCGGGAG	862
QY	349	CTTGGACACCATACCAATGATTTGATTTATGAGTTACAAAGCTTTTCCCTGGAAATGAA	408
Db	863	CCGGAGAGACCAATCCTTGTGAGTATGGAGTATGGAGTTACTCAGGCTTCCCTTCACACAGAG	922
QY	409	GAGGGGTAGAGTGGAGTCTCAAGCATACACACAGGTTGGAAGAAATGTGGACCT	468
Db	923	GAGGAGTGAAGTTGATTCACACGGTACAGCCACAGGTGGAAGAAATGTGGACTT	982
QY	469	TTTAAGGAGTAGACACAAAGAGCCAGCATGGGCCAAGCTCTCCAGATCTCAAGGG	528
Db	983	CTCAAGGGGTAGACACGAGCAGCAGCGTGGGCCAAGCTCTCCAGATCTCAAGGG	1042
QY	529	TTCACTGACCTGCTACTGATGACGAGCAGGAGCAATAACACCCAGATAGAGGAGCAG	588
Db	1043	TTCAAGAGCTGCTGCTGATGATGGCAGGAGCAATAACACCTCAGATCGAGGAGTACA	1102
QY	589	GATCACAATTACTACATTTCTCGGATATATGTTCCAGCGGATTCGCCAGCGGGATCTG	648
Db	1103	GACCACAATTACTATATATCTCGAATATATGTTCCATCTGATCTGCCAGCGGGATTTA	1162
QY	649	TGGTTTAACATAGACCAATGGAAAAGACAAAGTGAAGATTCACGGGATACTTCCAAAC	708
Db	1163	TGGGTGACATACACCAATGGAAAAGATAAAGTGAAGATTCATGGAATTTGTCCAAT	1222
QY	709	ACTCATCGGCAAGCTGCAAGAGTGAATCTGCTCGATTTTCCATTTATGATGCTATTT	768
Db	1223	ACTCATCGGCAAGCTGCAAGAGTGAATCTGCTCGATTTTCCATTTATGATGCTATTT	1282
QY	769	CTAAATGAAGTCACTGTGGCACTGGGGGTTTCATATATACGGAGAGTGTACATCGA	828
Db	1283	CTACGTGAATCACTGTGGCACTGGGGGTTTCATATATACGGAGAGTGTACATCGA	1342
QY	829	ATGCTCACACTACACAGATATAGTCTCTTTAATGGCAAAATTTGATCCAGTGTATCC	888
Db	1343	ATGCTAACAGCCACACAGATATAGTCTCTTTAATGGCAAAATTTGATCCAGTGTATCC	1402
QY	889	AGAAATTCAACTGCAGATATTTGATATGGCAGAGCTTTGTTGTCCAGTGGGACCAT	948
Db	1403	AGAAATTCAACTGCAGATATTTGATATGGCAGAGCTTTGTTGTCCAGTGGGACCAT	1462
QY	949	GTCCACCTCGAGGATTAATTAACACCTGGGAAGTTTCAATTCAGGCCACACTCCTCATG	1008
Db	1463	GTACATCTCCAGGATTAATTAACCTGGGAAGTTTCAATTCAGGCCACACTCCTCATG	1522
QY	1009	GACGGGGCATCATCTTTGGATACAAAGAAATCCCTGCTTGGTCCACAGATAGTTCT	1068
Db	1523	GATGGAGCAATCATCTTTGGATACAAAGAAATCCCTGCTTGGTCCACAGATAGTTCT	1582
QY	1069	ACCAACCTCAGTGAAGTGGGTTGATGATGCAATTTGCTGGTCCACAGGATCCAG	1128
Db	1583	ACCAATCATCCAGTGAAGTGGGTTGATGATGCAATTTGCTGGTCCACAGGATCCAG	1642
QY	1129	CAAAATCCCAATGTTCCGAAGAACAAATTTATGATATACCGAGTAGAATACAAATG	1188
Db	1643	CAAAATCCCAATGTTCCGAAGAACAAATTTATGATATACCGAGTAGAATACAAATG	1702
QY	1189	TCCAAATTAACACATCTCAGCTGGGATGAGTACCTCCACATGCTCCAGTTTC	1248
Db	1703	TCAAAATTAACACATCTCAGCTGGGATGAGTACCTCCACATGCTCCAGTTTC	1762
QY	1249	AATGGTTGGCCCTTGTGTTCTCCAGATTTGTTTCAACTGCAAGTGGTGGTGCACAAA	1308
Db	1763	AACAGATGGCCCTTGTGTTCTTCTCAGATTTGTTTCAACTGCAAGTGGTGGTGCACAAA	1822

QY	1309	CTTCAAAGATGCTCCAGTGGATTTGATCCCATCGGAGGACTGGGTGGACAGTGGATGC	1368
Db	1823	CTTCAAAGATGTTCCAGTGGATTTGATCGTCATCGGAGGACTGGGTGGACAGTGGATGC	1882
QY	1369	CCGGAGAGGTACACTCAAAGAGAGATGTGTGAGAGACAGAGCCAGGAGAGA--CA	1425
Db	1883	CCTGAAG-----AGTCAAAGAGAGAGATGTGTGAGAAATACAGAACCACTGGAACCTCT	1936
QY	1426	TCTCAAACCTACACAGACCTCCACACAGACCCACCATGCAATTCAGGGTCTCCAGCACCA	1485
Db	1937	TCTCGAACCCACCAACCATAGAGGCGACAAACCCAGTTCAGGGTCTCTAACTACCACC	1996
QY	1486	AGAGAGCTGTGACATCTCAGATGCTACAGCTCCAGCCCTGCTACAGAGATGACACGAAGTA	1545
Db	1997	AGAAGAGCAGTCACTCTCAGTTTCCACAGCCCTCCCTACAGAGATGATACCAAGATA	2056
QY	1546	GCCTACATCTCAAAGACAGAGTGGAGCCCTCCACAGATGACAGTGCAGCTGAGAAGAAAGGA	1605
Db	2057	GCATACATCTAAAGATAATGAGCTTCTACAGATGACAGTGCAGCTGAGAAGAAAGGG	2116
QY	1606	GGACCTCATGAGGCTCTCAATTTGGAATTCATCTTGGTCTCTATATAGCAGCG	1665
Db	2117	GGACCTCATGAGGCTCTCAATTTGGAATTCATCTTGGTCTCTATATAGCAGCG	2176
QY	1666	GCCATTTCTGGTGCAGCTGTATATGTATCACCATC	1699
Db	2177	GCCATTTCTGGTGCAGCTGTATATGTATCACCACC	2210

Search completed: June 23, 2003, 19:45:44
Job time : 494 secs